Jeffrey W Harper

List of Publications by Year in Descending Order

223 papers	48,685 citations	99 h-index	220 g-index
251 ext. papers	55,923 ext. citations	20.6 avg, IF	7.43 L-index

#	Paper	IF	Citations
223	Brain-derived autophagosome profiling reveals the engulfment of nucleoid-enriched mitochondrial fragments by basal autophagy in neurons.. *Neuron*, **2022**,	13.9	5
222	Mechanisms underlying ubiquitin-driven selective mitochondrial and bacterial autophagy.. *Molecular Cell*, **2022**,	17.6	4
221	A multi-scale map of cell structure fusing protein images and interactions. *Nature*, **2021**,	50.4	9
220	Global ubiquitylation analysis of mitochondria in primary neurons identifies endogenous Parkin targets following activation of PINK1. *Science Advances*, **2021**, 7, eabj0722	14.3	5
219	Temporal proteomics during neurogenesis reveals large-scale proteome and organelle remodeling via selective autophagy. *Molecular Cell*, **2021**,	17.6	9
218	ORF10-Cullin-2-ZYG11B complex is not required for SARS-CoV-2 infection. *Proceedings of the National Academy of Sciences of the United States of America*, **2021**, 118,	11.5	8
217	Dual proteome-scale networks reveal cell-specific remodeling of the human interactome. *Cell*, **2021** , 184, 3022-3040.e28	56.2	86
216	Cullin-RING Ubiquitin Ligase Regulatory Circuits: A Quarter Century Beyond the F-Box Hypothesis. *Annual Review of Biochemistry*, **2021**, 90, 403-429	29.1	17
215	Quantitative intravital imaging in zebrafish reveals dynamics of physiological-stress-induced mitophagy. *Journal of Cell Science*, **2021**, 134,	5.3	12
214	Super Heavy TMTpro Labeling Reagent: An Alternative and Higher-Charge-State-Amenable Stable-Isotope-Labeled TMTpro Variant. *Journal of Proteome Research*, **2021**, 20, 3009-3013	5.6	1
213	iRQC, a surveillance pathway for 40S ribosomal quality control during mRNA translation initiation. *Cell Reports*, **2021**, 36, 109642	10.6	1
212	Quantitative proteomics reveals the selectivity of ubiquitin-binding autophagy receptors in the turnover of damaged lysosomes by lysophagy. *ELife*, **2021**, 10,	8.9	8
211	Functional conservation and divergence of the helix-turn-helix motif of E2 ubiquitin-conjugating enzymes.. *EMBO Journal*, **2021**, e108823	13	0
210	Ubiquitin chain-elongating enzyme UBE2S activates the RING E3 ligase APC/C for substrate priming. *Nature Structural and Molecular Biology*, **2020**, 27, 550-560	17.6	9
209	Global Landscape and Dynamics of Parkin and USP30-Dependent Ubiquitylomes in iNeurons during Mitophagic Signaling. *Molecular Cell*, **2020**, 77, 1124-1142.e10	17.6	69
208	Systematic quantitative analysis of ribosome inventory during nutrient stress. *Nature*, **2020**, 583, 303-309	50.4	24
207	Inhibition of sphingolipid synthesis improves outcomes and survival in GARP mutant mice, a model of motor neuron degeneration. *Proceedings of the National Academy of Sciences of the United States of America*, **2020**, 117, 10565-10574	11.5	6

206	EDF1 coordinates cellular responses to ribosome collisions. *ELife*, **2020**, 9,	8.9	27
205	Pathogenic Pathways in Early-Onset Autosomal Recessive Parkinson's Disease Discovered Using Isogenic Human Dopaminergic Neurons. *Stem Cell Reports*, **2020**, 14, 75-90	8	18
204	The endoplasmic reticulum P5A-ATPase is a transmembrane helix dislocase. *Science*, **2020**, 369,	33.3	43
203	Ribosome Abundance Control Via the Ubiquitin-Proteasome System and Autophagy. *Journal of Molecular Biology*, **2020**, 432, 170-184	6.5	33
202	Mitochondrial Reprogramming Underlies Resistance to BCL-2 Inhibition in Lymphoid Malignancies. *Cancer Cell*, **2019**, 36, 369-384.e13	24.3	107
201	Protein aggregation mediates stoichiometry of protein complexes in aneuploid cells. *Genes and Development*, **2019**, 33, 1031-1047	12.6	42
200	TEX264 Is an Endoplasmic Reticulum-Resident ATG8-Interacting Protein Critical for ER Remodeling during Nutrient Stress. *Molecular Cell*, **2019**, 74, 891-908.e10	17.6	115
199	Probing the Global Cellular Responses to Lipotoxicity Caused by Saturated Fatty Acids. *Molecular Cell*, **2019**, 74, 32-44.e8	17.6	84
198	Excessive Cell Growth Causes Cytoplasm Dilution And Contributes to Senescence. *Cell*, **2019**, 176, 1083-1097.e18	36.2	144
197	The PINK1 kinase-driven ubiquitin ligase Parkin promotes mitochondrial protein import through the presequence pathway in living cells. *Scientific Reports*, **2019**, 9, 11829	4.9	29
196	Mutations in RABL3 alter KRAS prenylation and are associated with hereditary pancreatic cancer. *Nature Genetics*, **2019**, 51, 1308-1314	36.3	31
195	Hook3 is a scaffold for the opposite-polarity microtubule-based motors cytoplasmic dynein-1 and KIF1C. *Journal of Cell Biology*, **2019**, 218, 2982-3001	7.3	25
194	ARIH2 Is a Vif-Dependent Regulator of CUL5-Mediated APOBEC3G Degradation in HIV Infection. *Cell Host and Microbe*, **2019**, 26, 86-99.e7	23.4	23
193	A glycine-specific N-degron pathway mediates the quality control of protein -myristoylation. *Science*, **2019**, 365,	33.3	62
192	The role of nuclear receptor co-activator 4 in erythropoiesis (Reply to Nai .). *Haematologica*, **2019**, 104, e585-e586	6.6	0
191	Integrated proteogenetic analysis reveals the landscape of a mitochondrial-autophagosome synapse during PARK2-dependent mitophagy. *Science Advances*, **2019**, 5, eaay4624	14.3	34
190	Mitotic regulators TPX2 and Aurora A protect DNA forks during replication stress by counteracting 53BP1 function. *Journal of Cell Biology*, **2019**, 218, 422-432	7.3	21
189	NCOA4 maintains murine erythropoiesis via cell autonomous and non-autonomous mechanisms. *Haematologica*, **2019**, 104, 1342-1354	6.6	20

188	Dynamics of PARKIN-Dependent Mitochondrial Ubiquitylation in Induced Neurons and Model Systems Revealed by Digital Snapshot Proteomics. *Molecular Cell*, **2018**, 70, 211-227.e8	17.6	95
187	Building and decoding ubiquitin chains for mitophagy. *Nature Reviews Molecular Cell Biology*, **2018**, 19, 93-108	48.7	277
186	Systematic Analysis of Human Cells Lacking ATG8 Proteins Uncovers Roles for GABARAPs and the CCZ1/MON1 Regulator C18orf8/RMC1 in Macroautophagic and Selective Autophagic Flux. *Molecular and Cellular Biology*, **2018**, 38,	4.8	62
185	BioPlex Display: An Interactive Suite for Large-Scale AP-MS Protein-Protein Interaction Data. *Journal of Proteome Research*, **2018**, 17, 722-726	5.6	21
184	Systematic analysis of ribophagy in human cells reveals bystander flux during selective autophagy. *Nature Cell Biology*, **2018**, 20, 135-143	23.4	92
183	RAB7A phosphorylation by TBK1 promotes mitophagy via the PINK-PARKIN pathway. *Science Advances*, **2018**, 4, eaav0443	14.3	70
182	Angelman syndrome-associated point mutations in the Zn-binding N-terminal (AZUL) domain of UBE3A ubiquitin ligase inhibit binding to the proteasome. *Journal of Biological Chemistry*, **2018**, 293, 18387-18399	5.4	20
181	Endosomal Rab cycles regulate Parkin-mediated mitophagy. *ELife*, **2018**, 7,	8.9	78
180	Biallelic Mutations in DNAJC12 Cause Hyperphenylalaninemia, Dystonia, and Intellectual Disability. *American Journal of Human Genetics*, **2017**, 100, 257-266	11	81
179	TIRR regulates 53BP1 by masking its histone methyl-lysine binding function. *Nature*, **2017**, 543, 211-216	50.4	61
178	G1 cyclins link proliferation, pluripotency and differentiation of embryonic stem cells. *Nature Cell Biology*, **2017**, 19, 177-188	23.4	76
177	TRAF2 and OTUD7B govern a ubiquitin-dependent switch that regulates mTORC2 signalling. *Nature* , **2017**, 545, 365-369	50.4	90
176	Architecture of the human interactome defines protein communities and disease networks. *Nature*, **2017**, 545, 505-509	50.4	755
175	Molecular definitions of autophagy and related processes. *EMBO Journal*, **2017**, 36, 1811-1836	13	857
174	Quantitative Phospho-proteomic Analysis of TNF/NF B Signaling Reveals a Role for RIPK1 Phosphorylation in Suppressing Necrotic Cell Death. *Molecular and Cellular Proteomics*, **2017**, 16, 1200-1216	7.6	13
173	SAMTOR is an -adenosylmethionine sensor for the mTORC1 pathway. *Science*, **2017**, 358, 813-818	33.3	235
172	Compensatory metabolic networks in pancreatic cancers upon perturbation of glutamine metabolism. *Nature Communications*, **2017**, 8, 15965	17.4	148
171	Blocking an N-terminal acetylation-dependent protein interaction inhibits an E3 ligase. *Nature Chemical Biology*, **2017**, 13, 850-857	11.7	56

170	Two Distinct Types of E3 Ligases Work in Unison to Regulate Substrate Ubiquitylation. *Cell*, **2016**, 166, 1198-1214.e24	56.2	106
169	Proteome complexity and the forces that drive proteome imbalance. *Nature*, **2016**, 537, 328-38	50.4	133
168	Endosome-ER Contacts Control Actin Nucleation and Retromer Function through VAP-Dependent Regulation of PI4P. *Cell*, **2016**, 166, 408-423	56.2	224
167	Cytokinesis involves a nontranscriptional function of the Hippo pathway effector YAP. *Science Signaling*, **2016**, 9, ra23	8.8	39
166	Mitochondrial Sirtuin Network Reveals Dynamic SIRT3-Dependent Deacetylation in Response to Membrane Depolarization. *Cell*, **2016**, 167, 985-1000.e21	56.2	157
165	Microcephaly Proteins Wdr62 and Aspm Define a Mother Centriole Complex Regulating Centriole Biogenesis, Apical Complex, and Cell Fate. *Neuron*, **2016**, 92, 813-828	13.9	82
164	Mitochondrial unfolded protein response controls matrix pre-RNA processing and translation. *Nature*, **2016**, 534, 710-3	50.4	152
163	Dual RING E3 Architectures Regulate Multiubiquitination and Ubiquitin Chain Elongation by APC/C. *Cell*, **2016**, 165, 1440-1453	56.2	91
162	Guidelines for the use and interpretation of assays for monitoring autophagy (3rd edition). *Autophagy*, **2016**, 12, 1-222	10.2	3838
161	System-Wide Modulation of HECT E3 Ligases with Selective Ubiquitin Variant Probes. *Molecular Cell* , **2016**, 62, 121-36	17.6	110
160	The CASTOR Proteins Are Arginine Sensors for the mTORC1 Pathway. *Cell*, **2016**, 165, 153-164	56.2	411
159	The MAP kinase pathway coordinates crossover designation with disassembly of synaptonemal complex proteins during meiosis. *ELife*, **2016**, 5, e12039	8.9	21
158	QIL1 mutation causes MICOS disassembly and early onset fatal mitochondrial encephalopathy with liver disease. *ELife*, **2016**, 5,	8.9	32
157	A protein interaction map for cell-cell adhesion regulators identifies DUSP23 as a novel phosphatase for □catenin. *Scientific Reports*, **2016**, 6, 27114	4.9	12
156	Phosphorylation of Atg9 regulates movement to the phagophore assembly site and the rate of autophagosome formation. *Autophagy*, **2016**, 12, 648-58	10.2	48
155	Highly Multiplexed Quantitative Mass Spectrometry Analysis of Ubiquitylomes. *Cell Systems*, **2016**, 3, 395-403.e4	10.6	115
154	Identification of TRIM27 as a novel degradation target of herpes simplex virus 1 ICP0. *Journal of Virology*, **2015**, 89, 220-9	6.6	29
153	Endogenous Parkin Preserves Dopaminergic Substantia Nigral Neurons following Mitochondrial DNA Mutagenic Stress. *Neuron*, **2015**, 87, 371-81	13.9	216

152	The BioPlex Network: A Systematic Exploration of the Human Interactome. *Cell*, **2015**, 162, 425-440	56.2	908
151	Defining roles of PARKIN and ubiquitin phosphorylation by PINK1 in mitochondrial quality control using a ubiquitin replacement strategy. *Proceedings of the National Academy of Sciences of the United States of America*, **2015**, 112, 6637-42	11.5	182
150	Systematic proteomics of the VCP-UBXD adaptor network identifies a role for UBXN10 in regulating ciliogenesis. *Nature Cell Biology*, **2015**, 17, 1356-69	23.4	49
149	The PINK1-PARKIN Mitochondrial Ubiquitylation Pathway Drives a Program of OPTN/NDP52 Recruitment and TBK1 Activation to Promote Mitophagy. *Molecular Cell*, **2015**, 60, 7-20	17.6	489
148	Proteomic analysis and identification of cellular interactors of the giant ubiquitin ligase HERC2. *Journal of Proteome Research*, **2015**, 14, 953-66	5.6	30
147	Ferritinophagy via NCOA4 is required for erythropoiesis and is regulated by iron dependent HERC2-mediated proteolysis. *ELife*, **2015**, 4,	8.9	195
146	Quantifying ubiquitin signaling. *Molecular Cell*, **2015**, 58, 660-76	17.6	104
145	A Systematic Analysis of Factors Localized to Damaged Chromatin Reveals PARP-Dependent Recruitment of Transcription Factors. *Cell Reports*, **2015**, 11, 1486-500	10.6	100
144	Exome sequencing in amyotrophic lateral sclerosis identifies risk genes and pathways. *Science*, **2015**, 347, 1436-41	33.3	642
143	QIL1 is a novel mitochondrial protein required for MICOS complex stability and cristae morphology. *ELife*, **2015**, 4,	8.9	104
142	Author response: Ferritinophagy via NCOA4 is required for erythropoiesis and is regulated by iron dependent HERC2-mediated proteolysis **2015**,		4
141	Quantitative proteomics identifies NCOA4 as the cargo receptor mediating ferritinophagy. *Nature*, **2014**, 509, 105-9	50.4	684
140	Spindle assembly factor protection. *Molecular Cell*, **2014**, 53, 165-6	17.6	2
139	Cyclin C is a haploinsufficient tumour suppressor. *Nature Cell Biology*, **2014**, 16, 1080-91	23.4	94
138	Structure of the DDB1-CRBN E3 ubiquitin ligase in complex with thalidomide. *Nature*, **2014**, 512, 49-53	50.4	508
137	Cell biology: balancing act. *Nature*, **2014**, 510, 347-8	50.4	5
136	Quantitative proteomics reveal a feedforward mechanism for mitochondrial PARKIN translocation and ubiquitin chain synthesis. *Molecular Cell*, **2014**, 56, 360-375	17.6	401
135	Structure of a RING E3 trapped in action reveals ligation mechanism for the ubiquitin-like protein NEDD8. *Cell*, **2014**, 157, 1671-84	56.2	121

134	TIF1β protein regulates epithelial-mesenchymal transition by operating as a small ubiquitin-like modifier (SUMO) E3 ligase for the transcriptional regulator SnoN1. *Journal of Biological Chemistry*, **2014**, 289, 25067-78	5.4	26
133	Treacher Collins syndrome TCOF1 protein cooperates with NBS1 in the DNA damage response. *Proceedings of the National Academy of Sciences of the United States of America*, **2014**, 111, 18631-6	11.5	64
132	TIMMDC1/C3orf1 functions as a membrane-embedded mitochondrial complex I assembly factor through association with the MCIA complex. *Molecular and Cellular Biology*, **2014**, 34, 847-61	4.8	69
131	Uba1 functions in Atg7- and Atg3-independent autophagy. *Nature Cell Biology*, **2013**, 15, 1067-78	23.4	130
130	Structural conservation of distinctive N-terminal acetylation-dependent interactions across a family of mammalian NEDD8 ligation enzymes. *Structure*, **2013**, 21, 42-53	5.2	72
129	The histone demethylase LSD1/KDM1A promotes the DNA damage response. *Journal of Cell Biology*, **2013**, 203, 457-70	7.3	80
128	A novel Hap1-Tsc1 interaction regulates neuronal mTORC1 signaling and morphogenesis in the brain. *Journal of Neuroscience*, **2013**, 33, 18015-21	6.6	13
127	Parallel SCF adaptor capture proteomics reveals a role for SCFFBXL17 in NRF2 activation via BACH1 repressor turnover. *Molecular Cell*, **2013**, 52, 9-24	17.6	71
126	Building and remodelling Cullin-RING E3 ubiquitin ligases. *EMBO Reports*, **2013**, 14, 1050-61	6.5	216
125	Landscape of the PARKIN-dependent ubiquitylome in response to mitochondrial depolarization. *Nature*, **2013**, 496, 372-6	50.4	689
124	Altered social behavior and neuronal development in mice lacking the Uba6-Use1 ubiquitin transfer system. *Molecular Cell*, **2013**, 50, 172-84	17.6	33
123	The X-linked intellectual disability protein PHF6 associates with the PAF1 complex and regulates neuronal migration in the mammalian brain. *Neuron*, **2013**, 78, 986-93	13.9	66
122	A high-confidence interaction map identifies SIRT1 as a mediator of acetylation of USP22 and the SAGA coactivator complex. *Molecular and Cellular Biology*, **2013**, 33, 1487-502	4.8	47
121	Landscape of the PARKIN-dependent ubiquitin modified proteome in response to mitochondrial depolarization defined through quantitative proteomics. *FASEB Journal*, **2013**, 27, 553.17	0.9	
120	Rab GTPase-activating proteins in autophagy: regulation of endocytic and autophagy pathways by direct binding to human ATG8 modifiers. *Molecular and Cellular Biology*, **2012**, 32, 1733-44	4.8	139
119	Comprehensive analysis of host cellular interactions with human papillomavirus E6 proteins identifies new E6 binding partners and reflects viral diversity. *Journal of Virology*, **2012**, 86, 13174-86	6.6	134
118	Cancer. Emerging anatomy of the BAP1 tumor suppressor system. *Science*, **2012**, 337, 1463-4	33.3	30
117	Guidelines for the use and interpretation of assays for monitoring autophagy. *Autophagy*, **2012**, 8, 445-544	10.2	2783

116	Systematic identification of interactions between host cell proteins and E7 oncoproteins from diverse human papillomaviruses. *Proceedings of the National Academy of Sciences of the United States of America*, **2012**, 109, E260-7	11.5	145
115	SLX-1 is required for maintaining genomic integrity and promoting meiotic noncrossovers in the Caenorhabditis elegans germline. *PLoS Genetics*, **2012**, 8, e1002888	6	38
114	Cutaneous human papillomavirus E6 proteins bind Mastermind-like coactivators and repress Notch signaling. *Proceedings of the National Academy of Sciences of the United States of America*, **2012**, 109, E1473-80	11.5	99
113	Identification and proteomic analysis of distinct UBE3A/E6AP protein complexes. *Molecular and Cellular Biology*, **2012**, 32, 3095-106	4.8	70
112	M phase phosphorylation of the epigenetic regulator UHRF1 regulates its physical association with the deubiquitylase USP7 and stability. *Proceedings of the National Academy of Sciences of the United States of America*, **2012**, 109, 4828-33	11.5	78
111	Understanding cullin-RING E3 biology through proteomics-based substrate identification. *Molecular and Cellular Proteomics*, **2012**, 11, 1541-50	7.6	57
110	Defining human ERAD networks through an integrative mapping strategy. *Nature Cell Biology*, **2011** , 14, 93-105	23.4	336
109	A DNA damage response screen identifies RHINO, a 9-1-1 and TopBP1 interacting protein required for ATR signaling. *Science*, **2011**, 332, 1313-7	33.3	163
108	Stuck in the middle: drugging the ubiquitin system at the e2 step. *Cell*, **2011**, 145, 1007-9	56.2	9
107	DNA unwinding by ASCC3 helicase is coupled to ALKBH3-dependent DNA alkylation repair and cancer cell proliferation. *Molecular Cell*, **2011**, 44, 373-84	17.6	129
106	Alternative ubiquitin activation/conjugation cascades interact with N-end rule ubiquitin ligases to control degradation of RGS proteins. *Molecular Cell*, **2011**, 43, 392-405	17.6	49
105	A genome-wide screen identifies p97 as an essential regulator of DNA damage-dependent CDT1 destruction. *Molecular Cell*, **2011**, 44, 72-84	17.6	89
104	Systematic and quantitative assessment of the ubiquitin-modified proteome. *Molecular Cell*, **2011**, 44, 325-40	17.6	1163
103	mTOR drives its own activation via SCF(βTrCP)-dependent degradation of the mTOR inhibitor DEPTOR. *Molecular Cell*, **2011**, 44, 290-303	17.6	191
102	Constructing and decoding unconventional ubiquitin chains. *Nature Structural and Molecular Biology*, **2011**, 18, 520-8	17.6	168
101	N-terminal acetylation acts as an avidity enhancer within an interconnected multiprotein complex. *Science*, **2011**, 334, 674-8	33.3	194
100	SCF(FBXO22) regulates histone H3 lysine 9 and 36 methylation levels by targeting histone demethylase KDM4A for ubiquitin-mediated proteasomal degradation. *Molecular and Cellular Biology*, **2011**, 31, 3687-99	4.8	72
99	Simply quantifying ubiquitin complexity. *Nature Methods*, **2011**, 8, 630-1	21.6	

98	The Brd4 extraterminal domain confers transcription activation independent of pTEFb by recruiting multiple proteins, including NSD3. *Molecular and Cellular Biology*, **2011**, 31, 2641-52	4.8	355
97	An OBSL1-Cul7Fbxw8 ubiquitin ligase signaling mechanism regulates Golgi morphology and dendrite patterning. *PLoS Biology*, **2011**, 9, e1001060	9.7	63
96	Network organization of the human autophagy system. *Nature*, **2010**, 466, 68-76	50.4	1185
95	Cdc25A and Dub3 in a high-stakes balancing act. *Nature Cell Biology*, **2010**, 12, 311-3	23.4	6
94	GEN1/Yen1 and the SLX4 complex: Solutions to the problem of Holliday junction resolution. *Genes and Development*, **2010**, 24, 521-36	12.6	74
93	NCoR1 mediates papillomavirus E8;E2C transcriptional repression. *Journal of Virology*, **2010**, 84, 4451-60	6.6	35
92	Genome-wide siRNA screen identifies SMCX, EP400, and Brd4 as E2-dependent regulators of human papillomavirus oncogene expression. *Proceedings of the National Academy of Sciences of the United States of America*, **2010**, 107, 3752-7	11.5	125
91	A genetic screen identifies FAN1, a Fanconi anemia-associated nuclease necessary for DNA interstrand crosslink repair. *Molecular Cell*, **2010**, 39, 36-47	17.6	261
90	Rictor forms a complex with Cullin-1 to promote SGK1 ubiquitination and destruction. *Molecular Cell*, **2010**, 39, 797-808	17.6	75
89	A genome-wide camptothecin sensitivity screen identifies a mammalian MMS22L-NFKBIL2 complex required for genomic stability. *Molecular Cell*, **2010**, 40, 645-57	17.6	81
88	Telomeric TuRF1 wars. *Developmental Cell*, **2010**, 18, 167-8	10.2	3
87	Ubiquitin gets CARDed. *Cell*, **2010**, 141, 220-2	56.2	3
86	Dynamics of cullin-RING ubiquitin ligase network revealed by systematic quantitative proteomics. *Cell*, **2010**, 143, 951-65	56.2	270
85	The Prp19 complex and the Usp4Sart3 deubiquitinating enzyme control reversible ubiquitination at the spliceosome. *Genes and Development*, **2010**, 24, 1434-47	12.6	170
84	Phosphorylation by casein kinase I promotes the turnover of the Mdm2 oncoprotein via the SCF(beta-TRCP) ubiquitin ligase. *Cancer Cell*, **2010**, 18, 147-59	24.3	164
83	Brd4 regulation of papillomavirus protein E2 stability. *Journal of Virology*, **2009**, 83, 8683-92	6.6	33
82	The SIOD disorder protein SMARCAL1 is an RPA-interacting protein involved in replication fork restart. *Genes and Development*, **2009**, 23, 2415-25	12.6	151
81	CDK inhibitors selectively diminish cell cycle controlled activation of the histone H4 gene promoter by p220NPAT and HiNF-P. *Journal of Cellular Physiology*, **2009**, 219, 438-48	7	13

80	Ubiquitin-like protein activation by E1 enzymes: the apex for downstream signalling pathways. *Nature Reviews Molecular Cell Biology*, **2009**, 10, 319-31	48.7	539
79	Perturbation of vacuolar maturation promotes listeriolysin O-independent vacuolar escape during Listeria monocytogenes infection of human cells. *Cellular Microbiology*, **2009**, 11, 1382-98	3.9	27
78	Defining the human deubiquitinating enzyme interaction landscape. *Cell*, **2009**, 138, 389-403	56.2	1163
77	Mammalian BTBD12/SLX4 assembles a Holliday junction resolvase and is required for DNA repair. *Cell*, **2009**, 138, 63-77	56.2	348
76	Structures of SPOP-substrate complexes: insights into molecular architectures of BTB-Cul3 ubiquitin ligases. *Molecular Cell*, **2009**, 36, 39-50	17.6	315
75	SCFbeta-TRCP controls oncogenic transformation and neural differentiation through REST degradation. *Nature*, **2008**, 452, 370-4	50.4	254
74	Cancer proliferation gene discovery through functional genomics. *Science*, **2008**, 319, 620-4	33.3	323
73	Staged assembly of histone gene expression machinery at subnuclear foci in the abbreviated cell cycle of human embryonic stem cells. *Proceedings of the National Academy of Sciences of the United States of America*, **2008**, 105, 16964-9	11.5	64
72	An FTS/Hook/p107(FHIP) complex interacts with and promotes endosomal clustering by the homotypic vacuolar protein sorting complex. *Molecular Biology of the Cell*, **2008**, 19, 5059-71	3.5	80
71	Regulation of postsynaptic RapGAP SPAR by Polo-like kinase 2 and the SCFbeta-TRCP ubiquitin ligase in hippocampal neurons. *Journal of Biological Chemistry*, **2008**, 283, 29424-32	5.4	46
70	Differential roles for checkpoint kinases in DNA damage-dependent degradation of the Cdc25A protein phosphatase. *Journal of Biological Chemistry*, **2008**, 283, 19322-8	5.4	43
69	Bortezomib-mediated inhibition of steroid receptor coactivator-3 degradation leads to activated Akt. *Clinical Cancer Research*, **2008**, 14, 7511-8	12.9	25
68	HiNF-P is a bifunctional regulator of cell cycle controlled histone H4 gene transcription. *Journal of Cellular Biochemistry*, **2007**, 101, 181-91	4.7	11
67	Cell cycle dependent phosphorylation and subnuclear organization of the histone gene regulator p220(NPAT) in human embryonic stem cells. *Journal of Cellular Physiology*, **2007**, 213, 9-17	7	53
66	A functional genomic screen identifies a role for TAO1 kinase in spindle-checkpoint signalling. *Nature Cell Biology*, **2007**, 9, 556-64	23.4	84
65	Dual E1 activation systems for ubiquitin differentially regulate E2 enzyme charging. *Nature*, **2007**, 447, 1135-8	50.4	260
64	Ubiquitin proteasome system (UPS): what can chromatin do for you?. *Current Opinion in Cell Biology*, **2007**, 19, 206-14	9	102
63	The tumor suppressor CYLD regulates entry into mitosis. *Proceedings of the National Academy of Sciences of the United States of America*, **2007**, 104, 8869-74	11.5	104

62	Human papillomavirus type 16 E7 oncoprotein associates with the cullin 2 ubiquitin ligase complex, which contributes to degradation of the retinoblastoma tumor suppressor. *Journal of Virology*, **2007**, 81, 9737-47	6.6	197
61	Structure of a Fbw7-Skp1-cyclin E complex: multisite-phosphorylated substrate recognition by SCF ubiquitin ligases. *Molecular Cell*, **2007**, 26, 131-43	17.6	339
60	The DNA damage response: ten years after. *Molecular Cell*, **2007**, 28, 739-45	17.6	1288
59	Anaphase initiation is regulated by antagonistic ubiquitination and deubiquitination activities. *Nature*, **2007**, 446, 876-81	50.4	299
58	DNA-damage control: Claspin destruction turns off the checkpoint. *Current Biology*, **2006**, 16, R932-4	6.3	11
57	The F-box protein FBX4 targets PIN2/TRF1 for ubiquitin-mediated degradation and regulates telomere maintenance. *Journal of Biological Chemistry*, **2006**, 281, 759-68	5.4	82
56	From loops to chains: unraveling the mysteries of polyubiquitin chain specificity and processivity. *ACS Chemical Biology*, **2006**, 1, 20-4	4.9	8
55	A calcium-regulated MEF2 sumoylation switch controls postsynaptic differentiation. *Science*, **2006**, 311, 1012-7	33.3	374
54	Structural complexity in ubiquitin recognition. *Cell*, **2006**, 124, 1133-6	56.2	115
53	A family of diverse Cul4-Ddb1-interacting proteins includes Cdt2, which is required for S phase destruction of the replication factor Cdt1. *Molecular Cell*, **2006**, 23, 709-21	17.6	476
52	Phosphorylation-dependent ubiquitination of cyclin D1 by the SCF(FBX4-alphaB crystallin) complex. *Molecular Cell*, **2006**, 24, 355-66	17.6	291
51	Drug discovery in the ubiquitin-proteasome system. *Nature Reviews Drug Discovery*, **2006**, 5, 596-613	64.1	468
50	Identification and functional evaluation of cellular and viral factors involved in the alteration of nuclear architecture during herpes simplex virus 1 infection. *Journal of Virology*, **2005**, 79, 12840-51	6.6	103
49	Control of lipid metabolism by phosphorylation-dependent degradation of the SREBP family of transcription factors by SCF(Fbw7). *Cell Metabolism*, **2005**, 1, 379-91	24.6	321
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